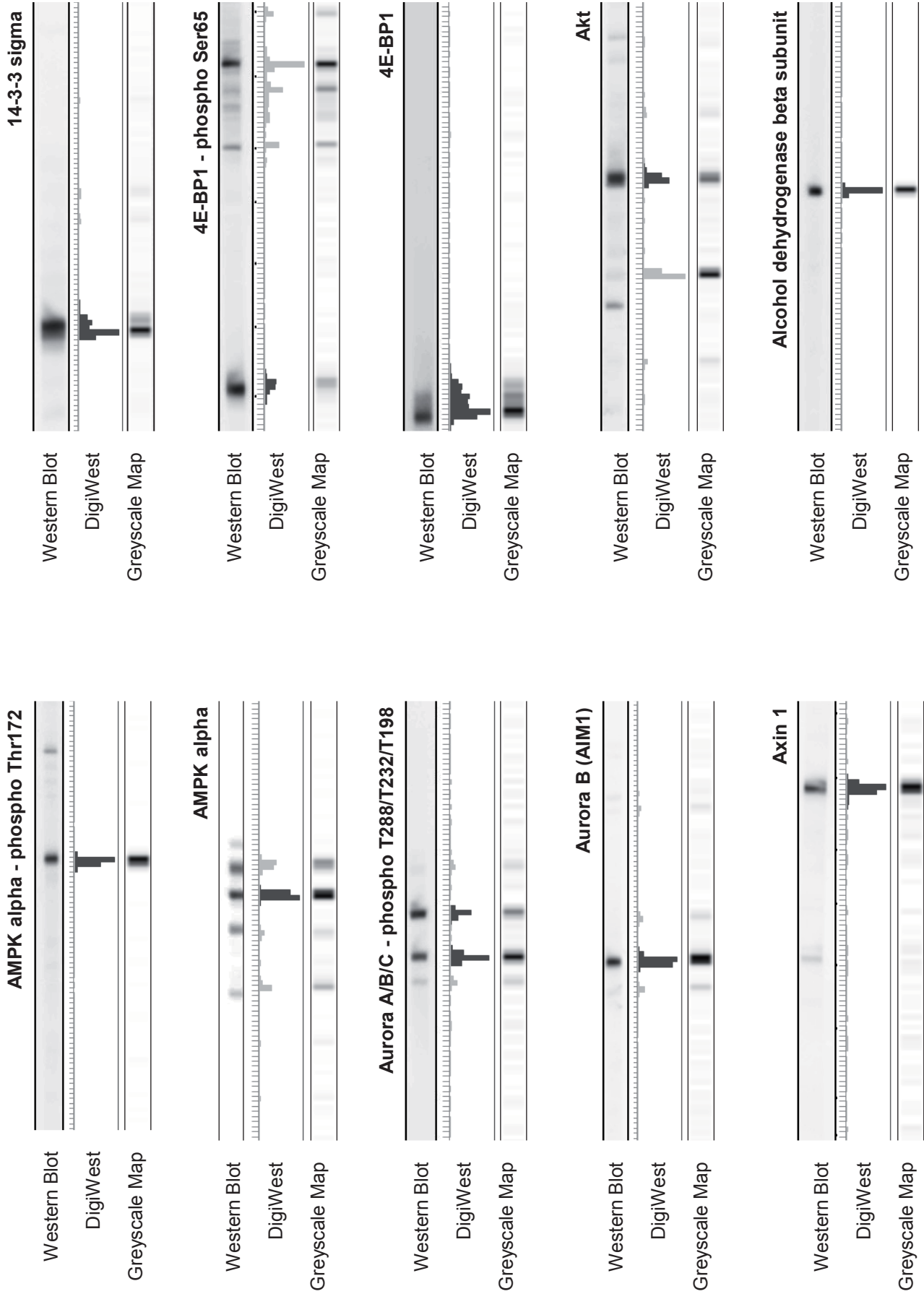
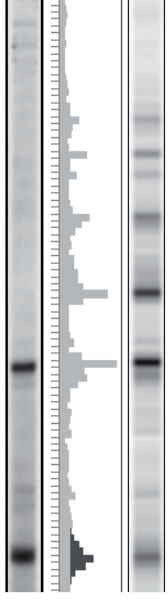


Supplementary figure 1: Comparison of DigiWest and Western blot.

20 µg of HepG2 lysate were processed using the described DigiWest procedure and aliquots of the generated bead pools were incubated with 104 commercially available antibodies; for comparison the same set of antibodies was used in standard Western blotting. Classical Western blot (left), DigiWest data, illustrated as a graph (middle) and grayscale maps (generated from numerical DigiWest data) are shown side by side for all tested antibodies. The antibodies in this set were selected to cover characteristics relevant for Western blotting: (i) single band antibodies and antibodies recognising multiple bands (ii) antibodies that result in high and in low signal, (iii) antibodies that detect proteins over the entire molecular weight range of the employed gel system, (iv) monoclonal and polyclonal antibodies and (v) antibodies recognizing soluble and membrane bound proteins. All Western blots we show in supplementary figure 1 were performed on one batch of HepG2 cells. N.B.: While Western blotting conditions and image acquisition for all these antibodies occurred under identical conditions, the employed protocol varies slightly from the described DigiWest workflow. Differences in buffer composition and a different blotting membrane (see methods section) contribute to the small differences seen in this comparison.

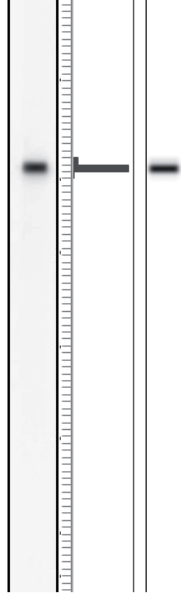


Bmf



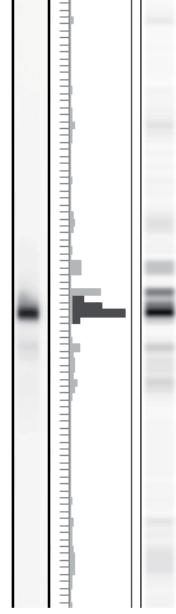
Western Blot
DigiWest
Greyscale Map

Calnexin



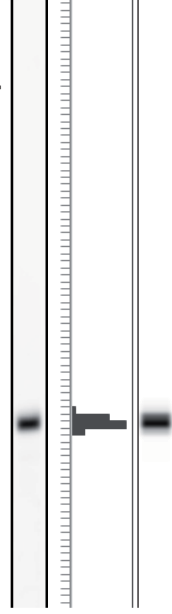
Western Blot
DigiWest
Greyscale Map

Caseinkinase 1 delta



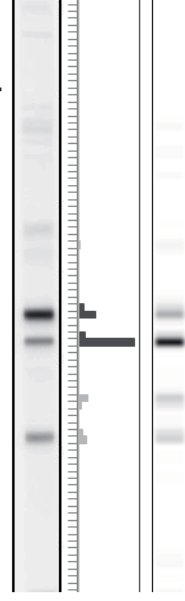
Western Blot
DigiWest
Greyscale Map

Caspase 3



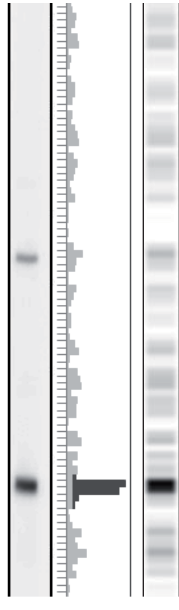
Western Blot
DigiWest
Greyscale Map

Caspase 9



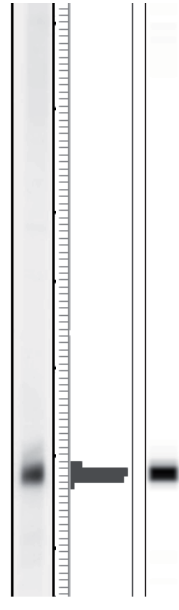
Western Blot
DigiWest
Greyscale Map

Bcl2



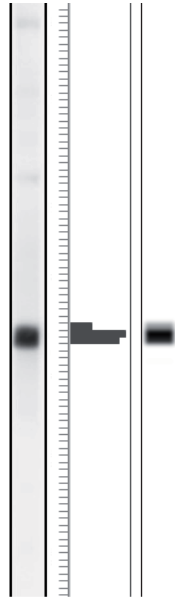
Western Blot
DigiWest
Greyscale Map

Bcl-xL



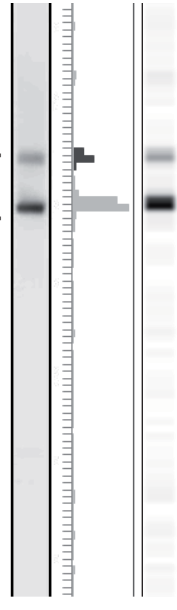
Western Blot
DigiWest
Greyscale Map

beta-Actin



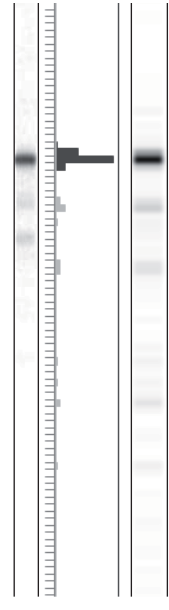
Western Blot
DigiWest
Greyscale Map

beta-Catenin - phospho Ser675



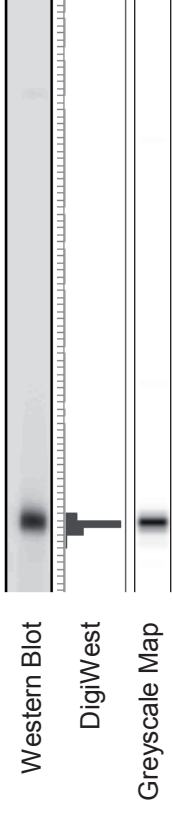
Western Blot
DigiWest
Greyscale Map

beta-Catenin

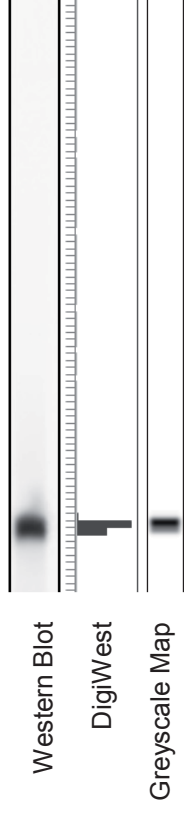


Western Blot
DigiWest
Greyscale Map

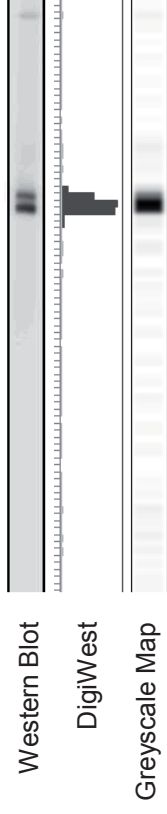
Cofilin - phospho Ser3



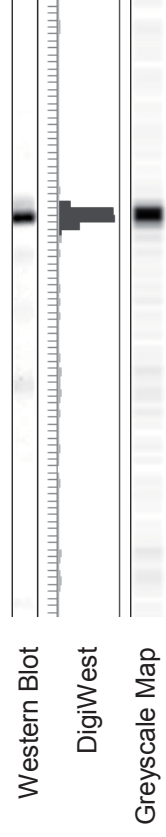
Cofilin



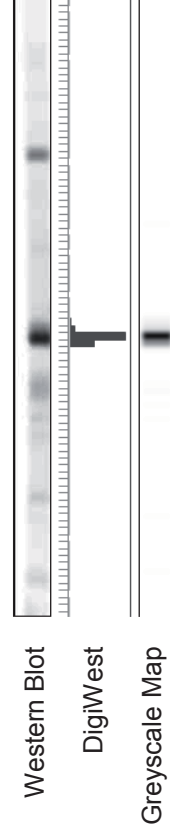
c-Raf - phospho Ser259



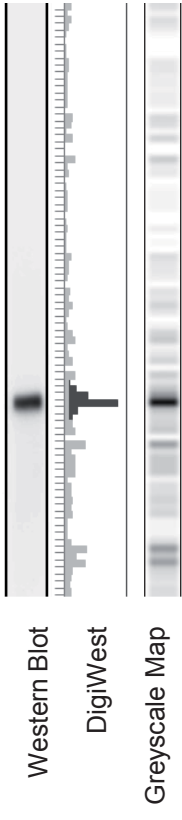
c-Raf



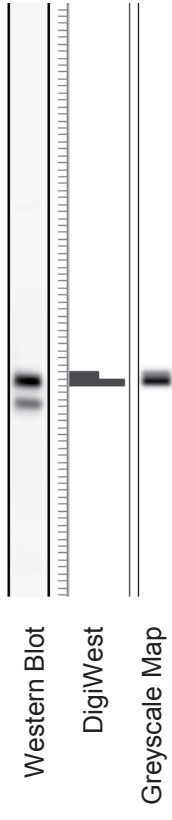
CREB - phospho Ser133



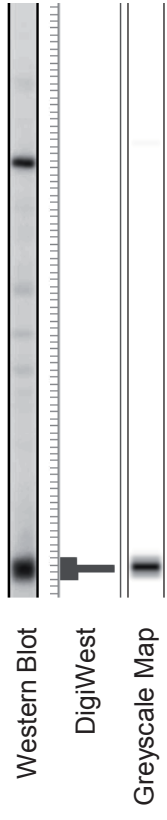
cdc2 - phospho Tyr15



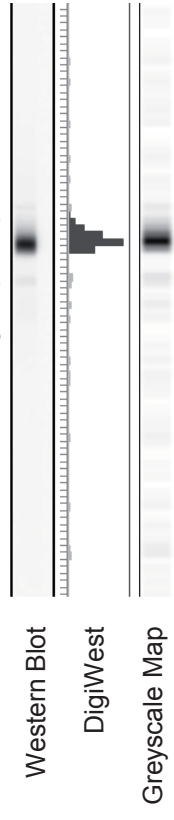
cdc2 (CDK1)



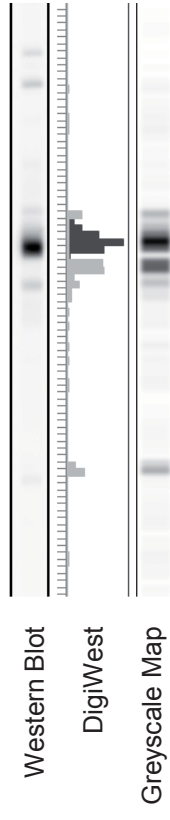
CDKN2B (p15 INK4B)

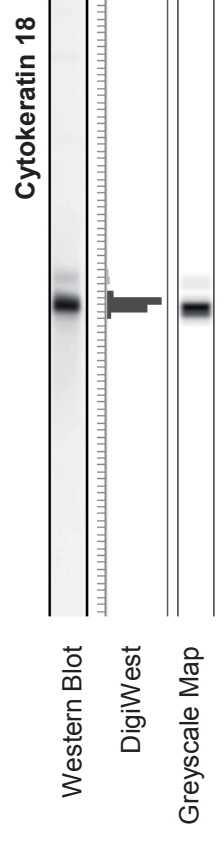
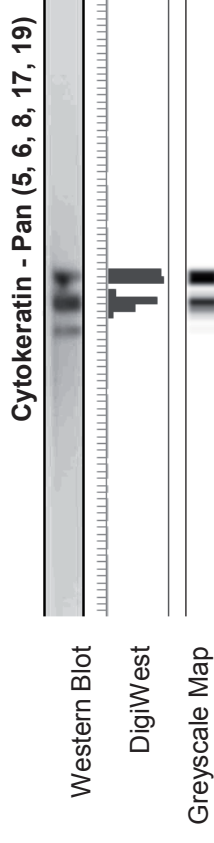
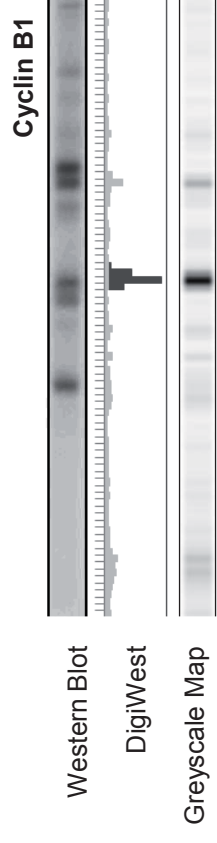
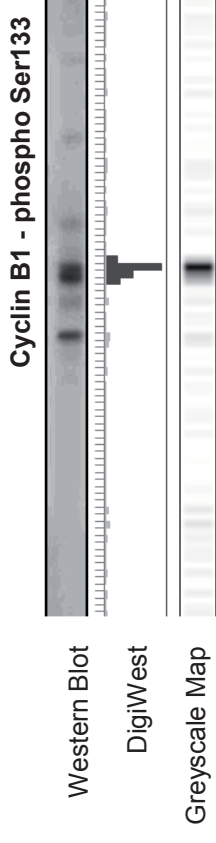
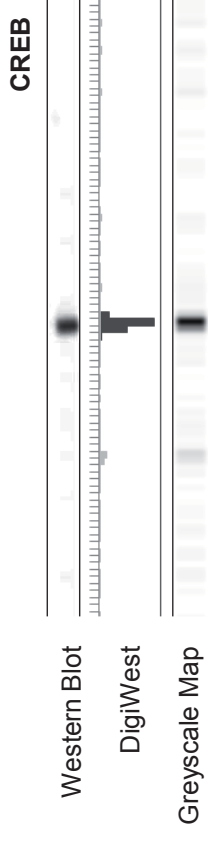
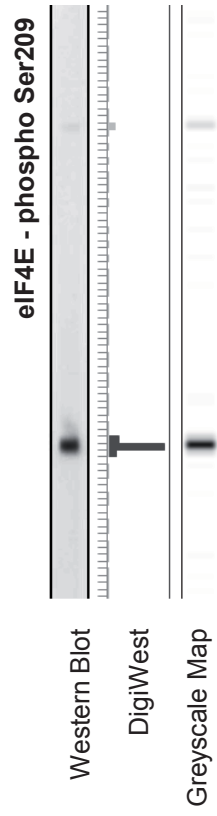
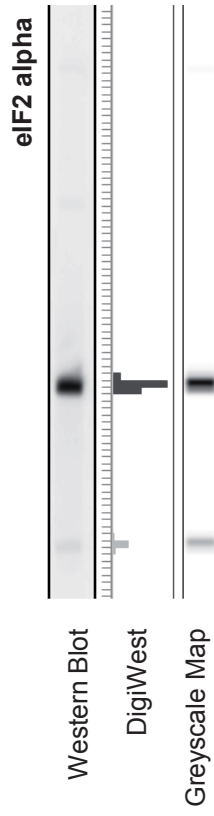
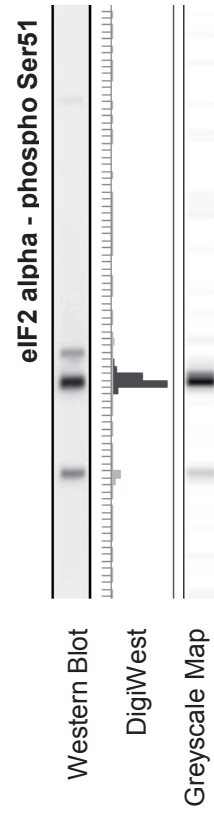
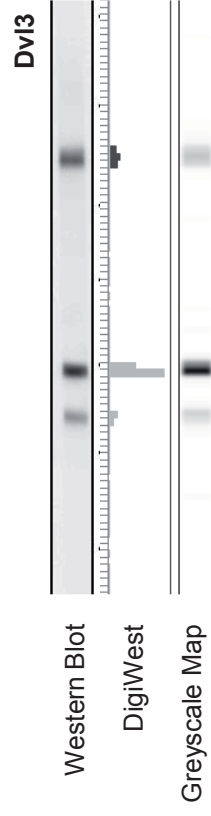
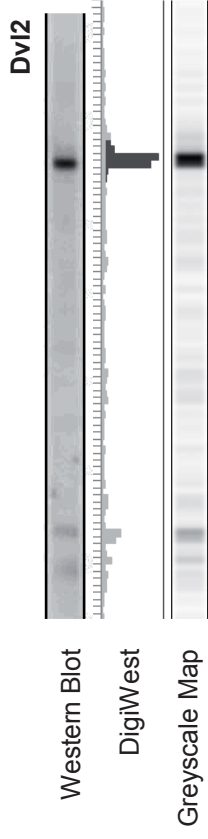


c-myc - phospho Thr58/Ser62

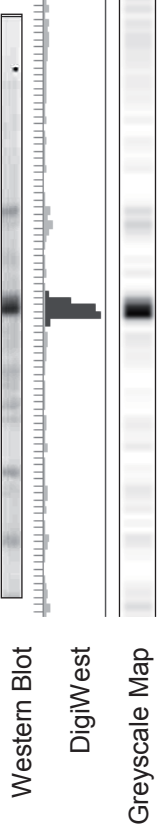


c-myc

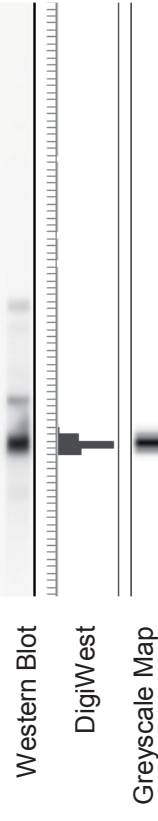




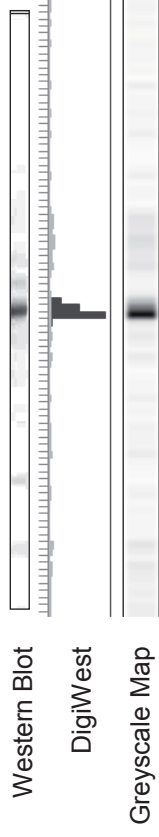
GSK3 beta - phospho Ser9



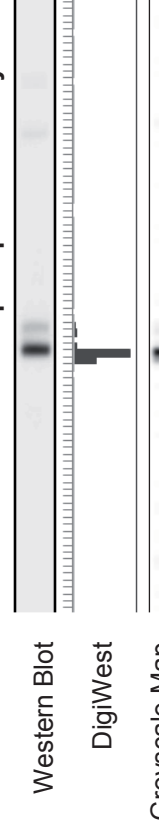
eIF4E



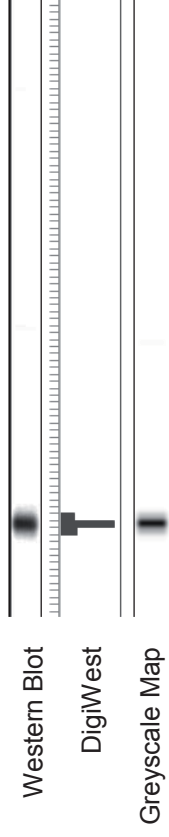
GSK3 beta



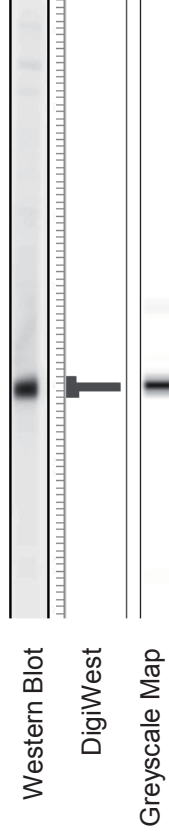
ERK1/2 phospho Thr202/Tyr204



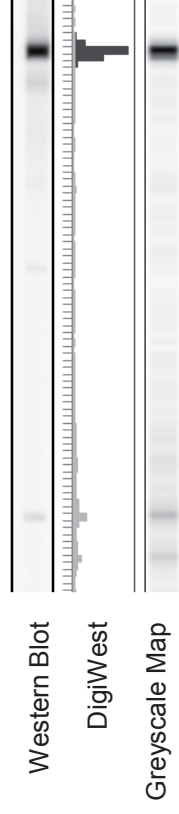
Ha-ras



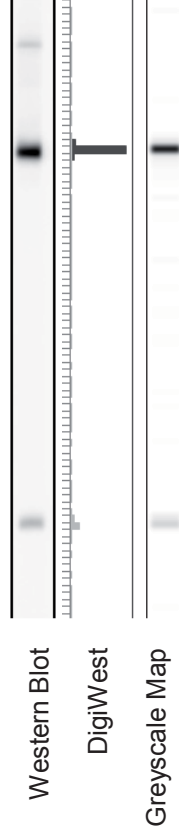
GAPDH



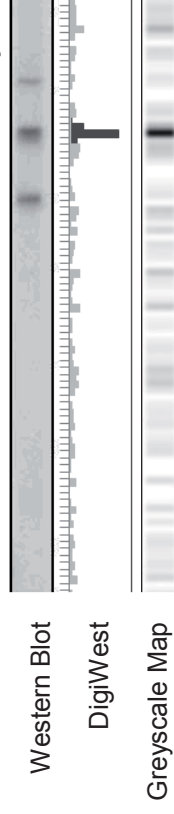
Her2



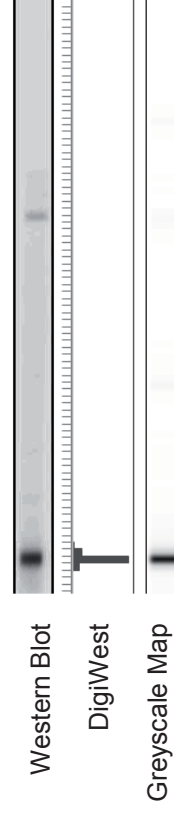
GCN5L2

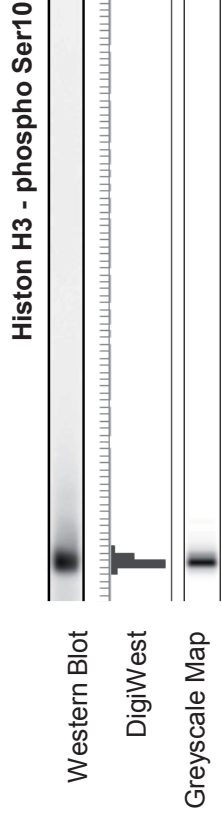
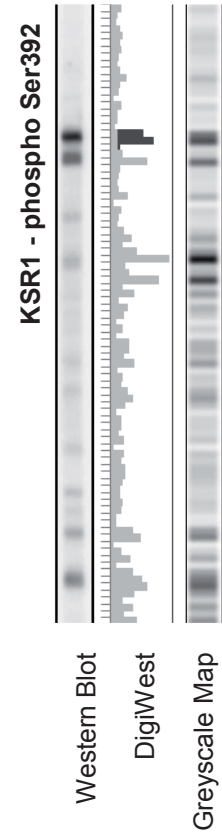
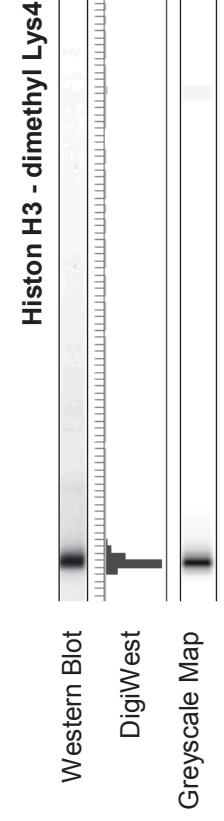
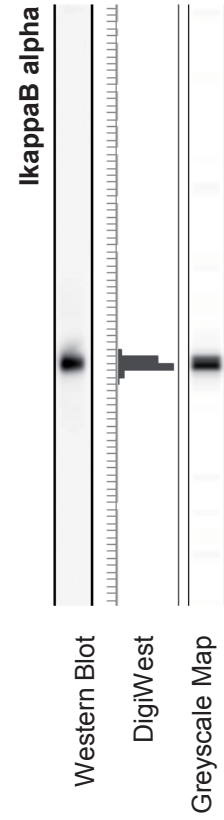
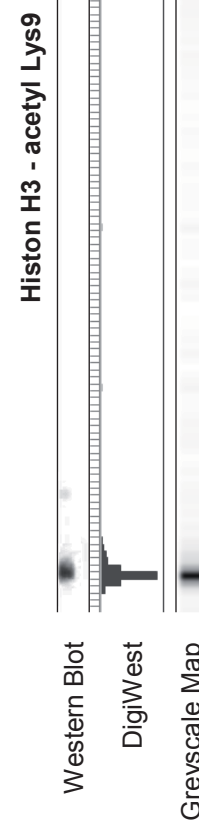
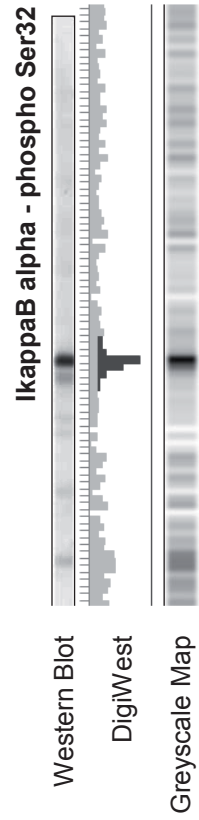
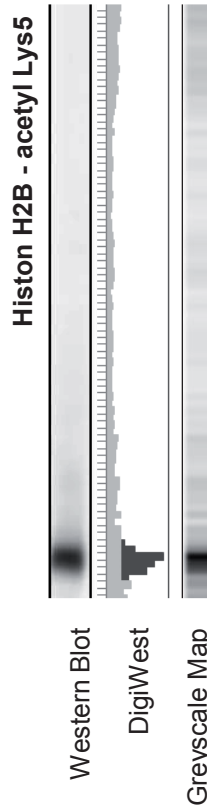
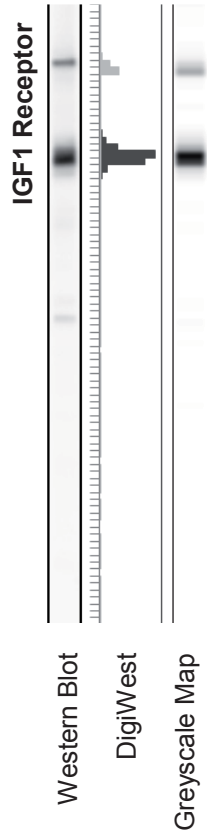
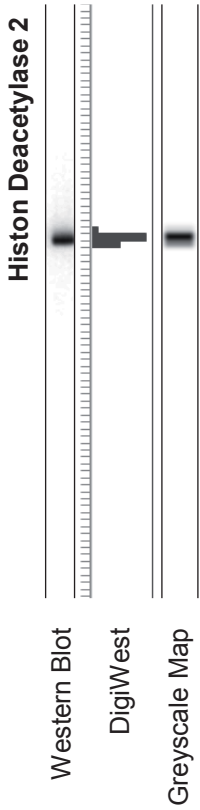
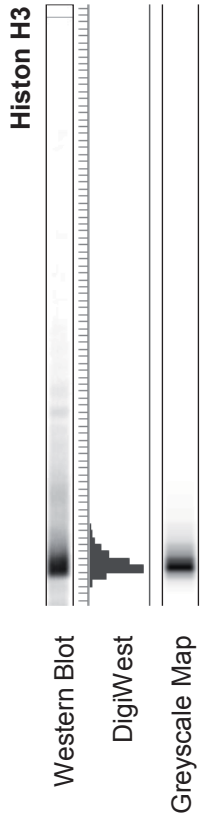


HIF1 alpha

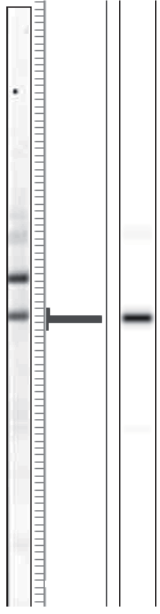


GDF3





MEK2

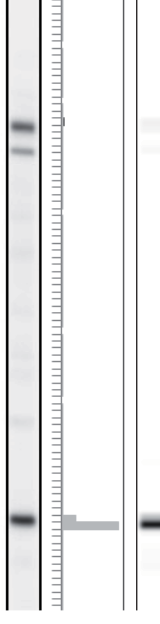


Western Blot

DigiWest

Greyscale Map

KSR1

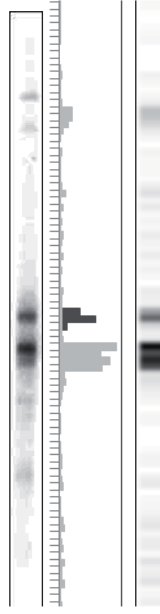


Western Blot

DigiWest

Greyscale Map

MKK4 - phospho Ser257/Thr261

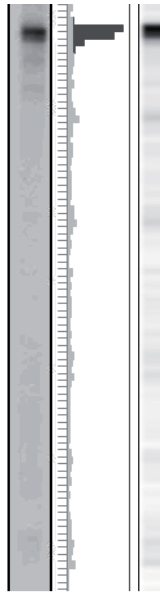


Western Blot

DigiWest

Greyscale Map

LRP6

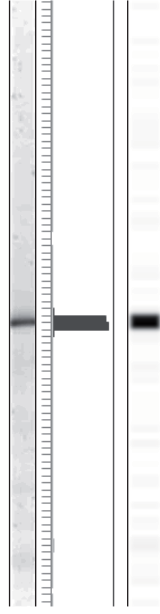


Western Blot

DigiWest

Greyscale Map

MKK4

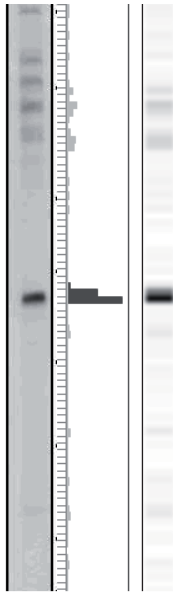


Western Blot

DigiWest

Greyscale Map

Mcl-1 - phospho Ser159/Thr163

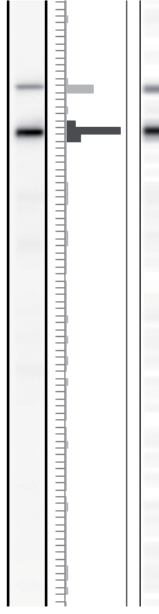


Western Blot

DigiWest

Greyscale Map

MLK3 (MAP3K11)

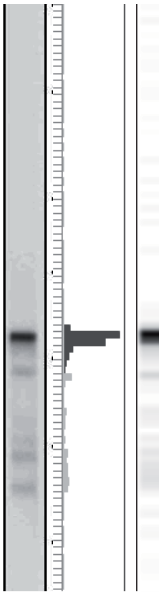


Western Blot

DigiWest

Greyscale Map

Mcl-1

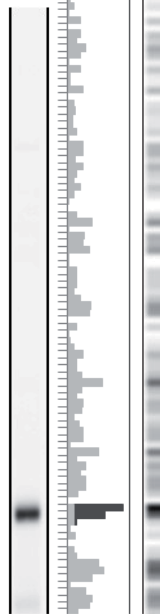


Western Blot

DigiWest

Greyscale Map

MOB1

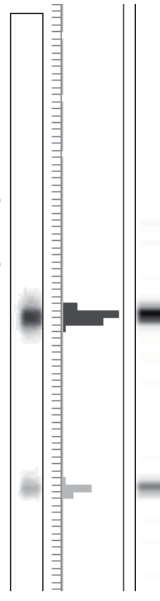


Western Blot

DigiWest

Greyscale Map

MEK1/2 - phospho Ser217/221

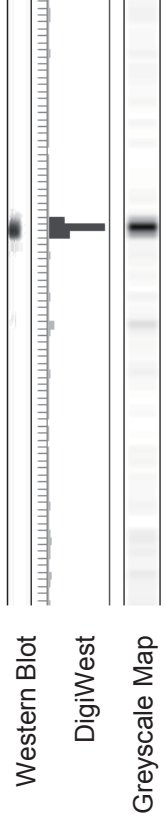


Western Blot

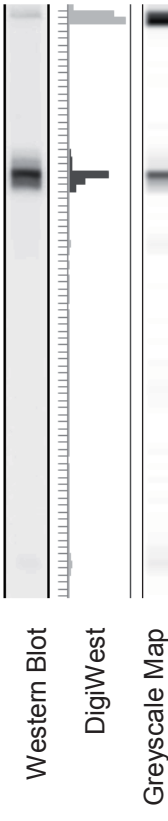
DigiWest

Greyscale Map

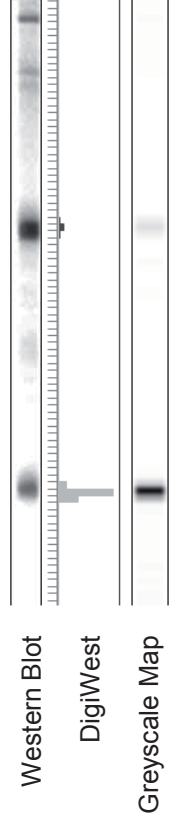
PAK 2



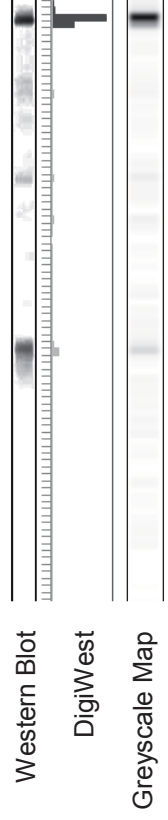
MSK1 - phospho Ser376



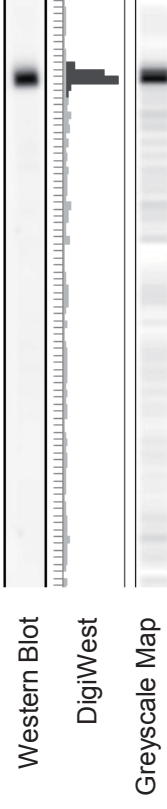
PAK1/2/3 - phospho Ser141



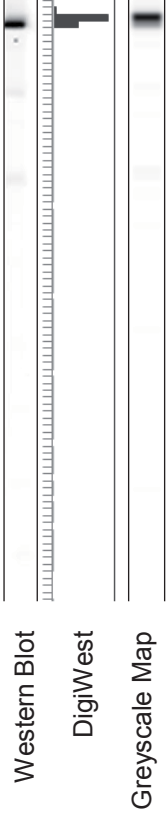
mTOR - phospho Ser2448



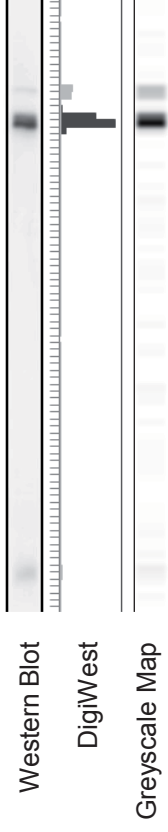
PERK



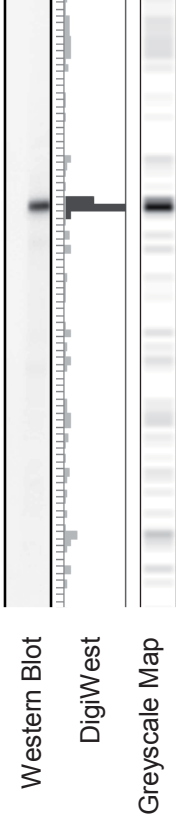
mTOR



PI3-kinase p110 beta



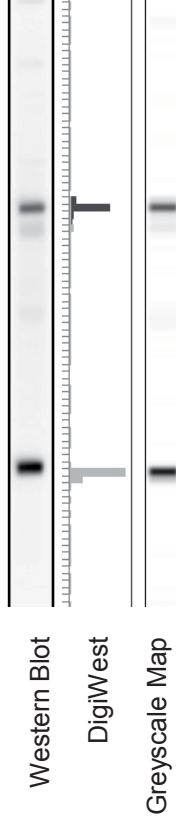
NF-κB p65 - phospho Ser536



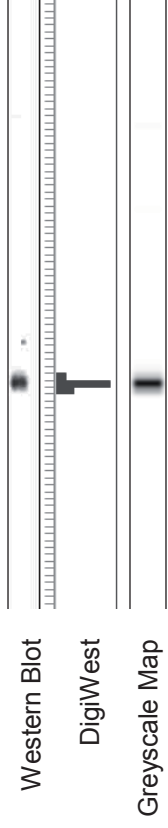
PKA C alpha



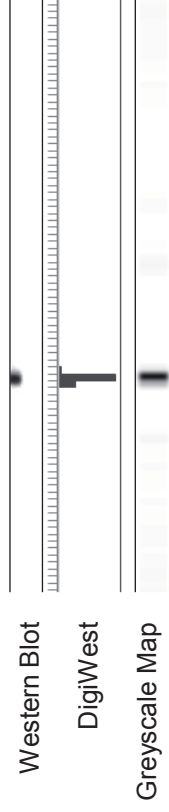
NF-κB p65



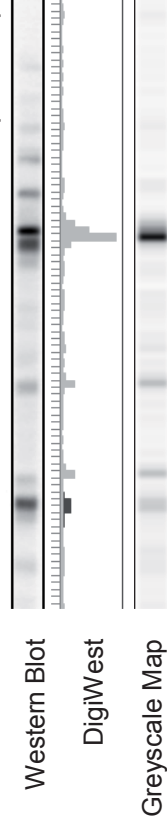
PP1 alpha - phospho Thr320



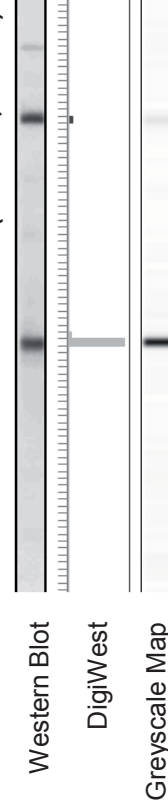
PP1 alpha



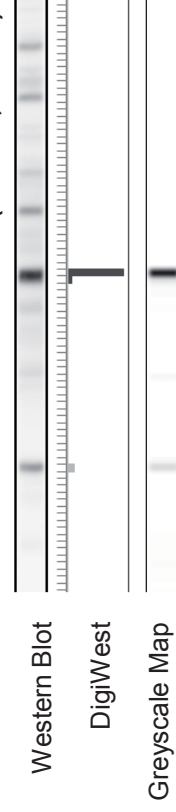
PRL-1 (PTP4A1)



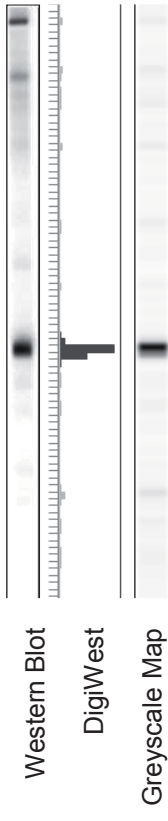
PTP-PEST (PTPN12, PTPN12)



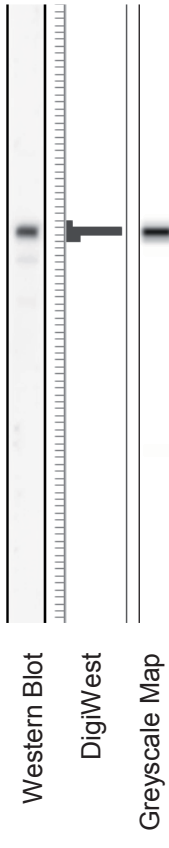
PTPRR (PTP-SL, PTP13)



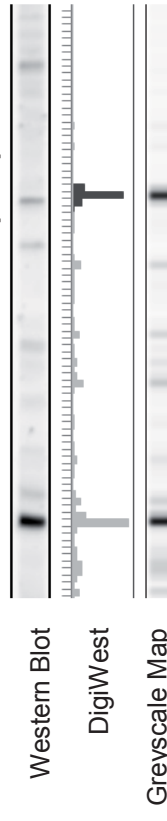
PKA C alpha/beta - phospho Thr197



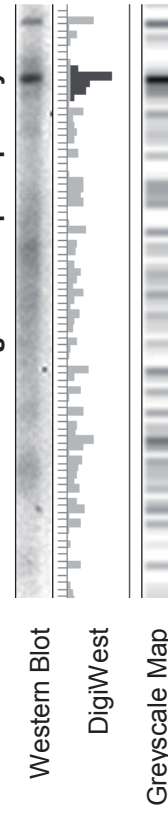
PKR



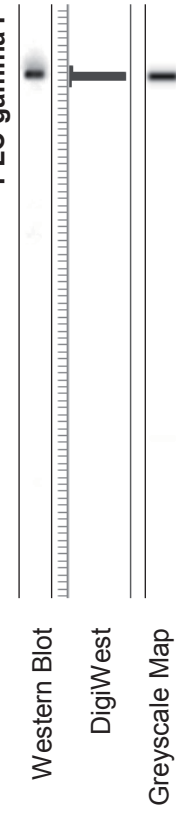
PKR - phospho Thr446



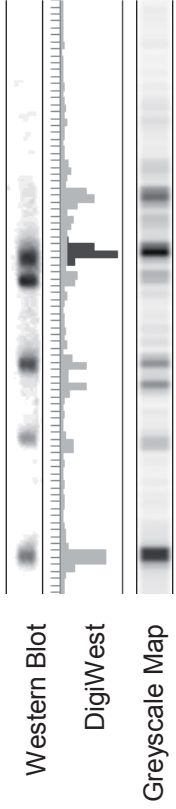
PLC gamma I - phospho Tyr783



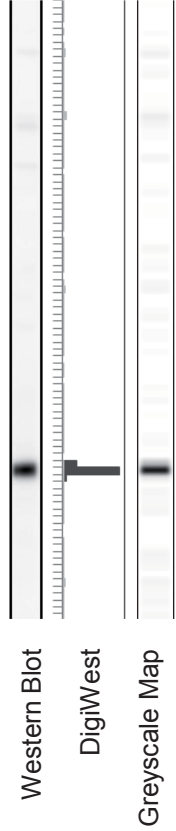
PLC gamma I



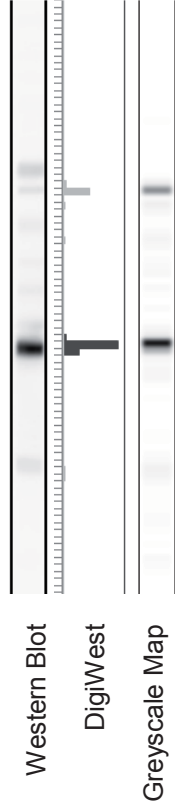
Smad2/3



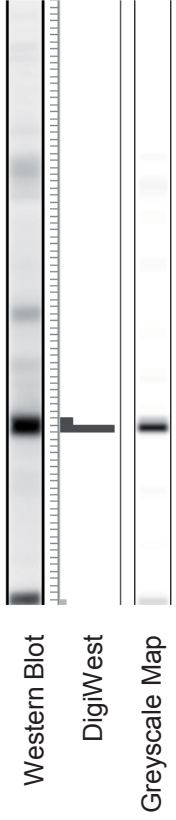
SOCS3



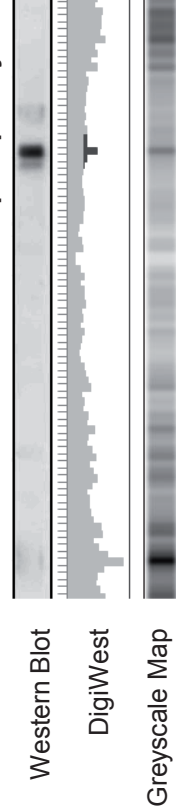
SPRY2 (Protein sprouty homolog 2)



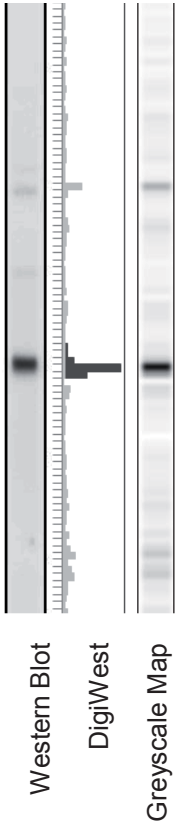
SPRY3 (Spry-3, Sprouty 3)



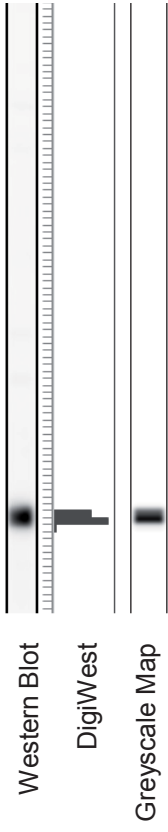
STAT 3 - phospho Tyr705



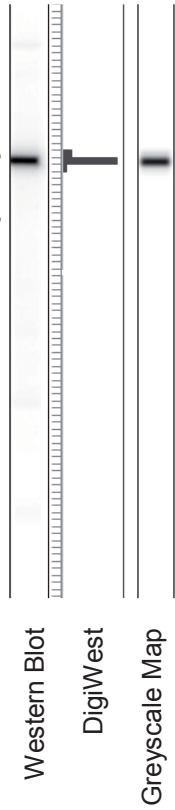
Rad51



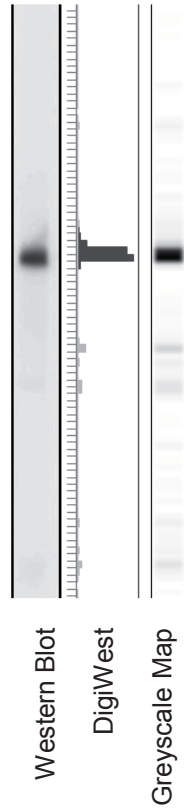
RKIP (PBP, PEBP, PEBP1)



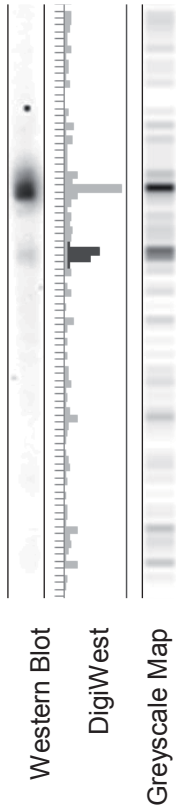
RSK 4 - phospho Ser235



Smad1



Smad2 - phospho Ser245/250/255

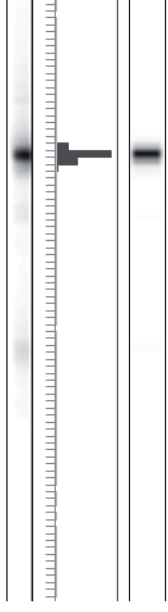


STAT 3

Western Blot

DigiWest

Greyscale Map

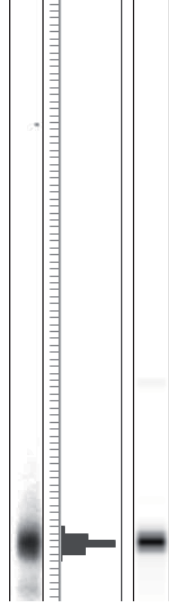


Superoxide dismutase (Cu/Zn)

Western Blot

DigiWest

Greyscale Map

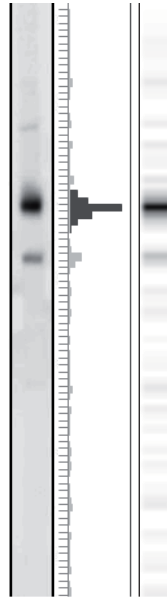


TAK1

Western Blot

DigiWest

Greyscale Map

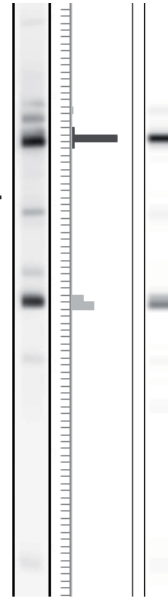


Topoisomerase 1

Western Blot

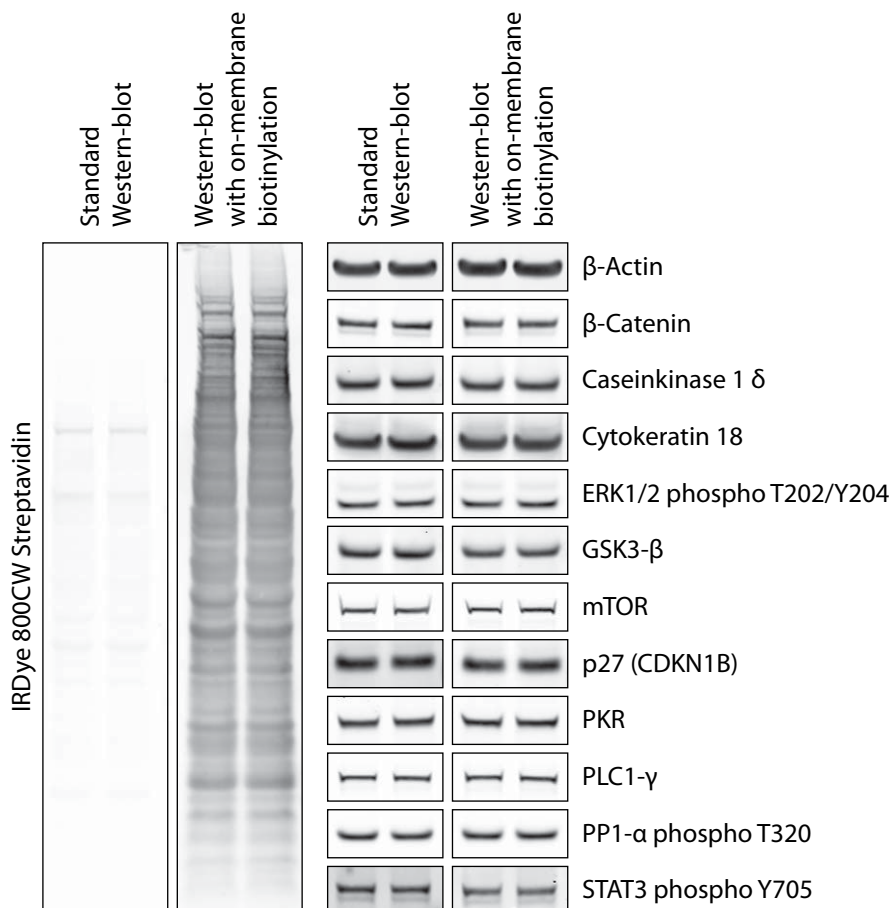
DigiWest

Greyscale Map



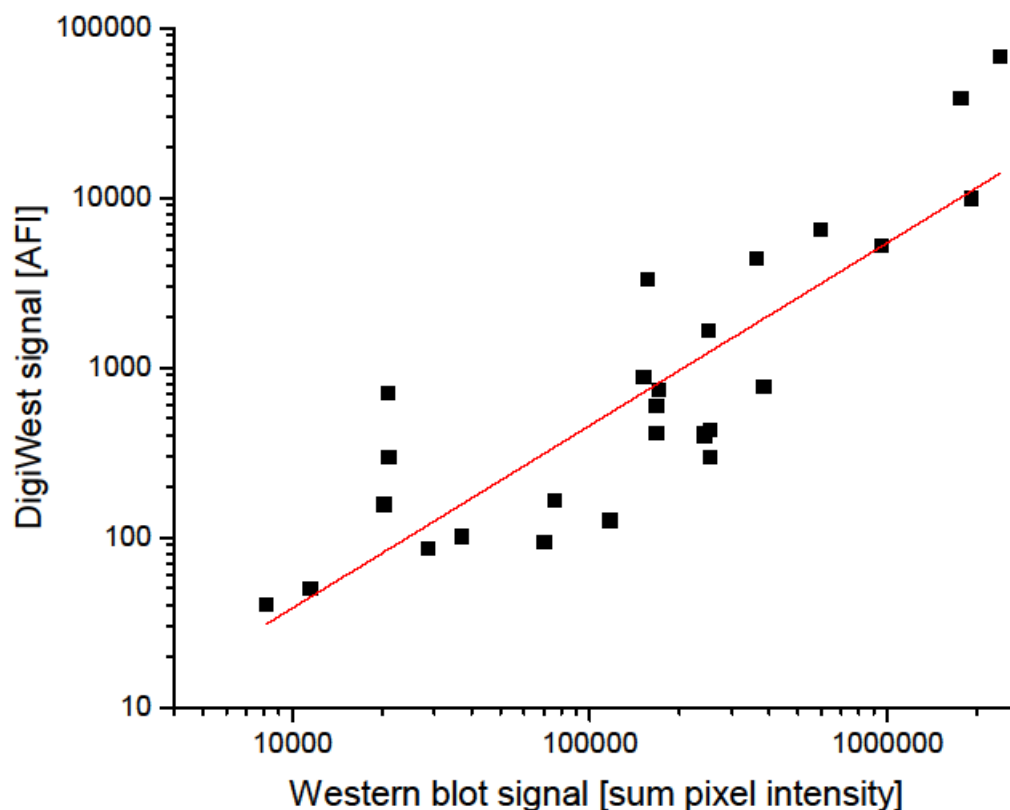
Supplementary figure 2: Effect of protein biotinylation on antibody binding during Western-blotting.

Western-blotting was performed under standard conditions and 20 µg HepG2 lysate were loaded per lane. Half of the Western-blot was processed under standard conditions, whereas the other half was subjected to the biotinylation step as performed in the DigiWest workflow. The Western-blotting was cut into blocks each containing 2 lanes and an antibody incubation was performed each using one block of a blot with and without biotinylation. Antibodies detecting proteins of different molecular weight and antibodies detecting phosphorylated proteins were used. To verify protein biotinylation, one block with and without biotinylation was incubated with IRDye800 labelled streptavidin. No differences in signal intensities for the 12 tested antibodies were detected, indicating that the biotinylation step that is performed during the DigiWest procedure does not influence antigenicity of the separated proteins and antibody recognition is not influenced.



Supplementary figure 3: Comparison of DigiWest and Western blot – Correlation analysis.

Correlation analysis between DigiWest peak intensities and Western blot band intensities was performed on expression data generated by the described DigiWest procedure and by a standardised Western blot protocol. Western blot band intensities were quantified using a near infrared fluorescence scanner as read-out system (see methods section). Proteins from mouse liver lysate (10 µg) were separated for DigiWest and for standard Western blotting, 30 antibodies (see supplementary figure 1) were used and the obtained numerical data were analysed. 2 antibodies gave no band in Western blotting whereas for 1 antibody no signal in DigiWest and Western blot was obtained. The signals generated for the remaining 27 antibodies were used for a correlation analysis and a Pearson correlation coefficient r of 0.86 was determined.



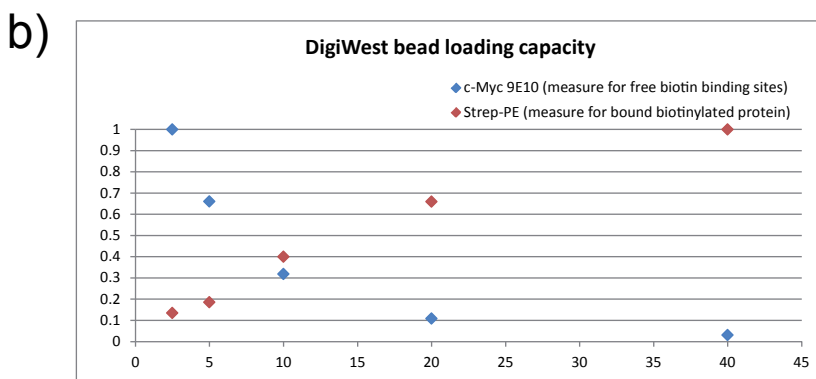
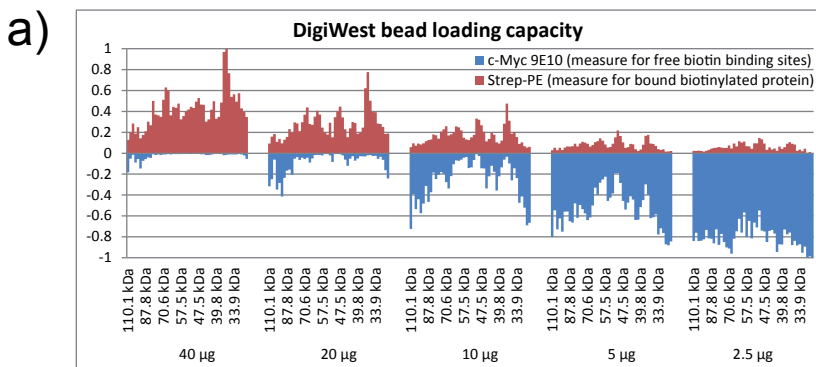
Supplementary figure 4: Binding capacity of Neutravidin coated beads.

To investigate the biotin binding capacity of the Neutravidin coated Luminex beads a DigiWest experiment was performed with a 1:2 dilution series of HepG2 lysate. 48 molecular weight fractions were generated from each Western blot lane covering the molecular weight range from 30 to 110 kDa containing most of the highly abundant proteins. After protein loading the DigiWest beads were incubated with a biotinylated peptide (c-Myc, Biotin-Doa-Doa-EQKLISEEDL) to occupy the remaining free biotin binding sites. The resulting bead mixes were either incubated with PE-labelled streptavidin or with an antibody detecting the peptide (c-Myc clone 9E10) and a PE-labelled secondary antibody. The signal obtained with PE-labelled streptavidin was used as a measure for bead-bound biotinylated proteins whereas the signal obtained with the c-Myc antibody was used as a measure for free biotin binding sites.

a) Signal obtained with PE-labelled streptavidin (red) normalized to the highest value and signal obtained with the c-Myc antibody (blue) normalized to the highest value (negative values). When 40 μ g HepG2 lysate are loaded saturation occurs based on the biotin-binding capacity.

b) Integrated signals normalized to the highest value.

Under the established DigiWest condition (amount of loaded protein 2.5 to 20 μ g) the binding capacity of the Neutravidin coated Luminex beads is in excess of biotinylated protein and thereby quantitative measurements are possible.



Supplementary figure 5: Protein binding capacity: Effect of increasing amounts of competing protein on signal intensity.

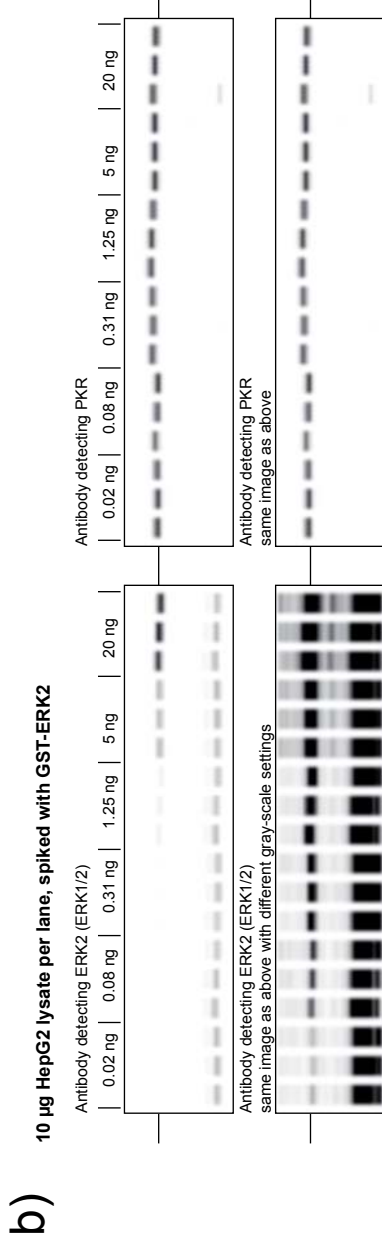
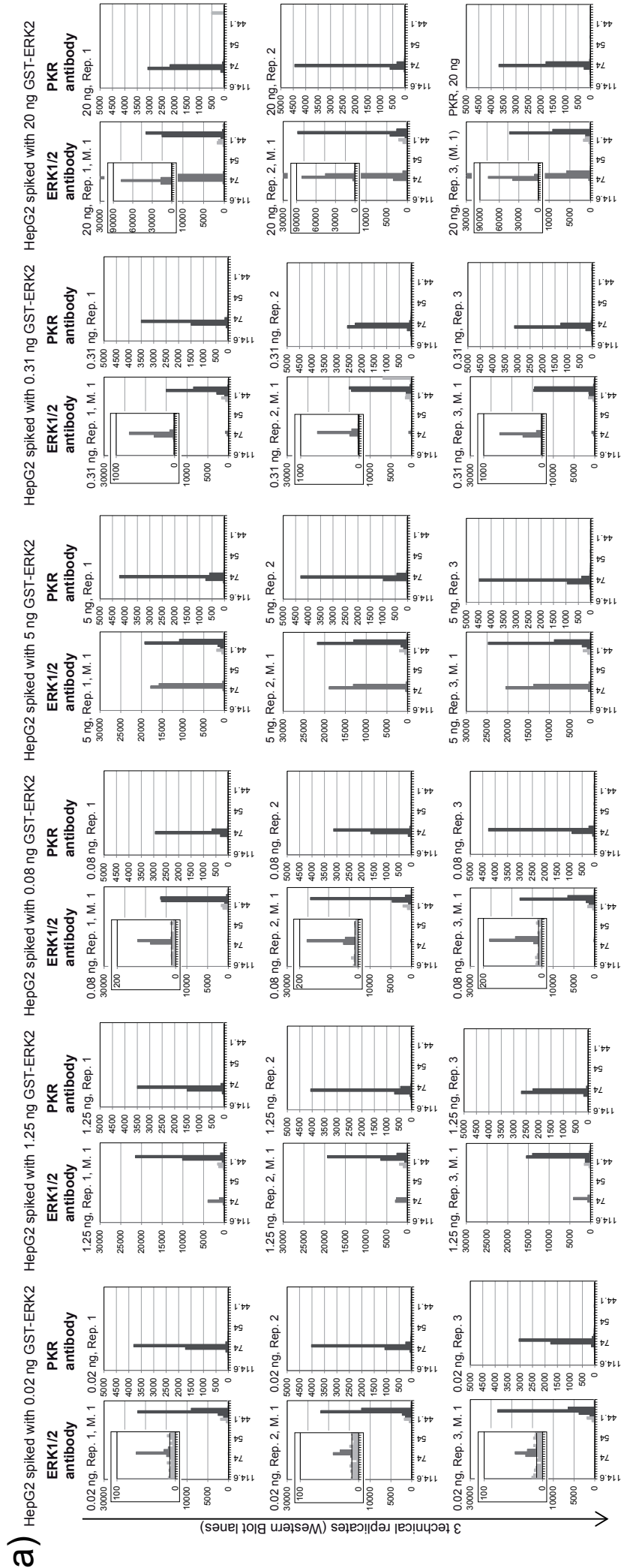
Beads obtained from the spike-in experiment (supplementary figure 2) were probed with an antibody recognizing PKR, a protein running exactly at the same molecular weight as GST-ERK2 (69 kDa) and signal was generated using standard conditions. Also shown is the signal generated with the ERK1/2 specific antibody for the samples spiked with GST-ERK2 (replicate 1 in supplementary figure 2).

a) Representation of obtained signal for the antibody directed against ERK1/2 as bar diagram; intrinsic ERK1 is highlighted in black, intrinsic ERK2 is highlighted in dark gray, spiked GST-ERK2 in medium gray (data also shown in supplementary figure 2) and data obtained with the antibody directed against PKR is shown in black.

b) Western-blot mimics (gray-scale maps generated from the Luminex data) representing the same data as in a).

The standard deviation of all integrals of the obtained PKR signals showed a CV of 8.8%; no competing effect was observed by increasing the amount of spiked protein. This experiment implies that quantitative measurements are possible since even a high amount of competing protein does not influence signal intensity of the protein of interest.

Supplementary figure 5

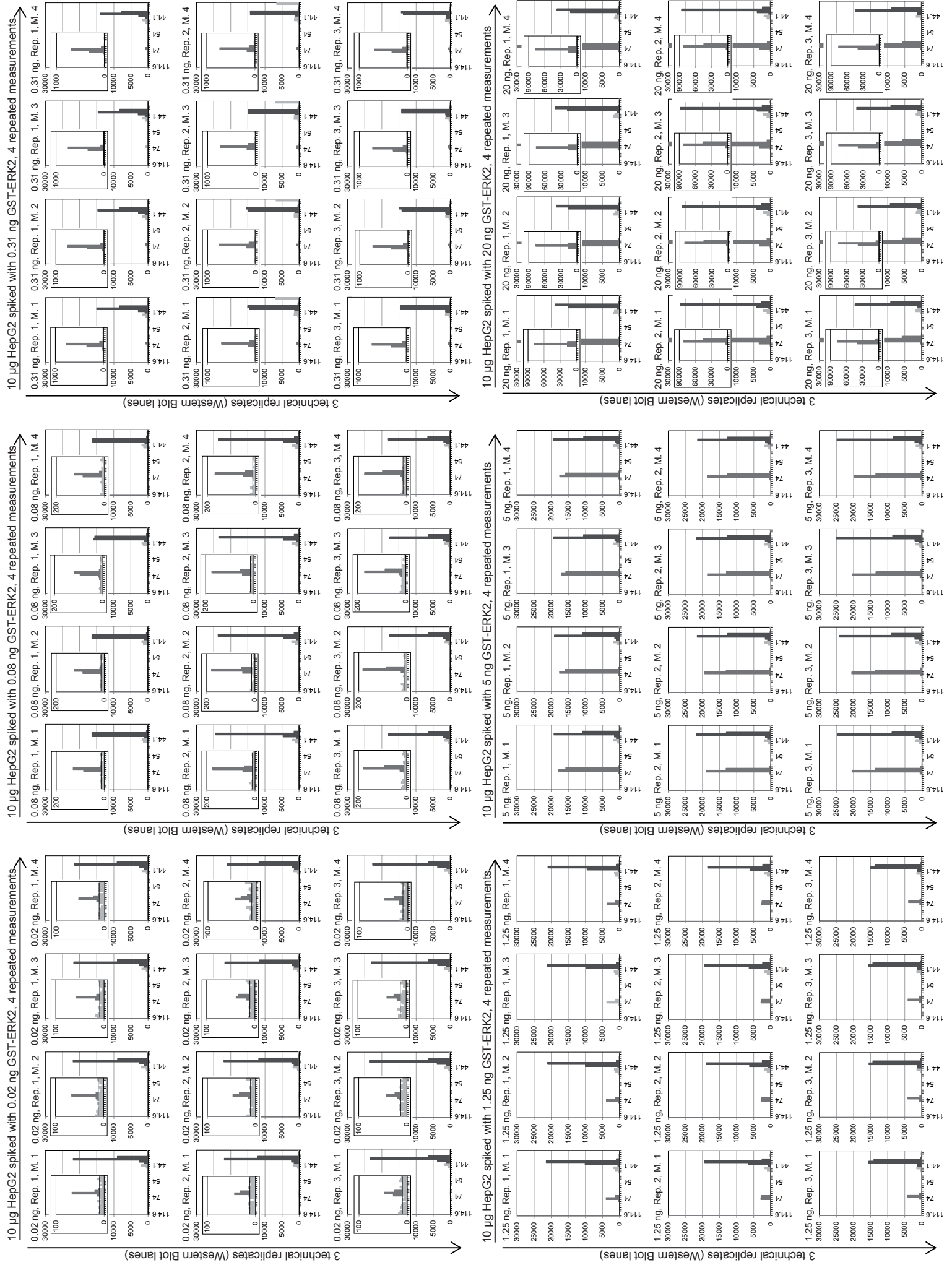


Supplementary figure 6: Spike-in experiment to determine sensitivity, linearity and reproducibility of DigiWest.

HepG2 lysate (10 µg per lane) was spiked with different amounts of GST-ERK2 (20 pg, 78 pg, 312 pg, 1.25 ng, 5 ng, 20 ng) and triplicate samples were generated. The 18 spiked samples were separated on three SDS-PAGE gels and DigiWest was performed for proteins with an apparent molecular weight between 40 kDa and 110 kDa. Bead-pools sufficient for 100 antibody incubations were prepared and aliquots were used for signal generation using an ERK1/2 specific antibody; measurements were repeated four times. The diagrams show intrinsic ERK2 highlighted in dark grey, GST-ERK2 in medium grey and ERK1 and remaining signal in light grey. Repeat measurements are shown from left to right whereas the technical replicates are shown from top to bottom.

The accompanying table shows the integrals of the identified peaks (GST-ERK2, intrinsic ERK2) obtained from DigiWest; the lower part of the table shows signal intensity obtained from quantification of the classical Western-Blot image.

Supplementary figure 6



DigiWest

GST-ERK2 quantification

(Spike-in per 10 µg HepG2 Lysate, relative signal)

	Replicate 1	Replicate 2	Replicate 3
20 ng Meas. 1	111610	132187	123061
Meas. 2	110545	131069	121013
Meas. 3	109539	133063	121319
Meas. 4	110796	132258	122093
5 ng Meas. 1	34446	32902	35241
Meas. 2	34452	33242	35176
Meas. 3	33635	32368	34849
Meas. 4	34339	32063	34365
1.25 ng Meas. 1	5458	5860	5568
Meas. 2	5339	5771	5471
Meas. 3	5212	5727	5450
Meas. 4	5095	5503	5178
0.31 ng Meas. 1	1208	993	1118
Meas. 2	1159	1051	1159
Meas. 3	1149	1046	1117
Meas. 4	1074	1006	1086
0.08 ng Meas. 1	217	241	270
Meas. 2	215	275	260
Meas. 3	228	252	264
Meas. 4	215	251	302
0.02 ng Meas. 1	85	60	73
Meas. 2	78	75	77
Meas. 3	67	64	74
Meas. 4	73	71	79

Mean	CV (%)
121546	7.58
33923	3.15
5469	4.37
1097	6.02
249	10.91
73	9.38

Mean	CV (%)
32399	9.57

Intrinsic ERK2

(in 10 µg HepG2 lysate, relative signal)

	Replicate 1	Replicate 2	Replicate 3
20 ng Meas. 1	34953	33795	29330
Meas. 2	34518	33194	28654
Meas. 3	35208	33441	28729
Meas. 4	33745	33003	30158
5 ng Meas. 1	32769	37621	35915
Meas. 2	32763	36971	35567
Meas. 3	32522	37395	36033
Meas. 4	32608	36794	35699
1.25 ng Meas. 1	33006	29025	32337
Meas. 2	32512	28286	32558
Meas. 3	32573	28731	32674
Meas. 4	31866	27581	31418
0.31 ng Meas. 1	27349	31321	32156
Meas. 2	26813	32022	31902
Meas. 3	26737	31581	31398
Meas. 4	25480	30164	30841
0.08 ng Meas. 1	33943	31263	27490
Meas. 2	34069	30510	27039
Meas. 3	32726	30317	27053
Meas. 4	33933	30173	27490
0.02 ng Meas. 1	34688	37989	34494
Meas. 2	34682	37824	34829
Meas. 3	34465	37132	34060
Meas. 4	34419	36704	33692

GST-ERK2 quantification

(Spike-in per 10 µg HepG2 Lysate, relative signal)

	Replicate 1	Replicate 2	Replicate 3
20 ng	318473100	329781002	
5 ng	135073639	134463994	
1.25 ng	36316470	36196382	
0.31 ng	8911814	9002800	9625102
0.08 ng	2586263	2532097	2636531
0.02 ng	1108895	1177614	924245

Mean	CV%
324127051	NA
134768817	NA
36256426	NA
9179905	4.23
2584964	2.02
1070252	12.24

Intrinsic ERK2 (in 10 µg HepG2 lysate)

(in 10 µg HepG2 lysate, relative signal)

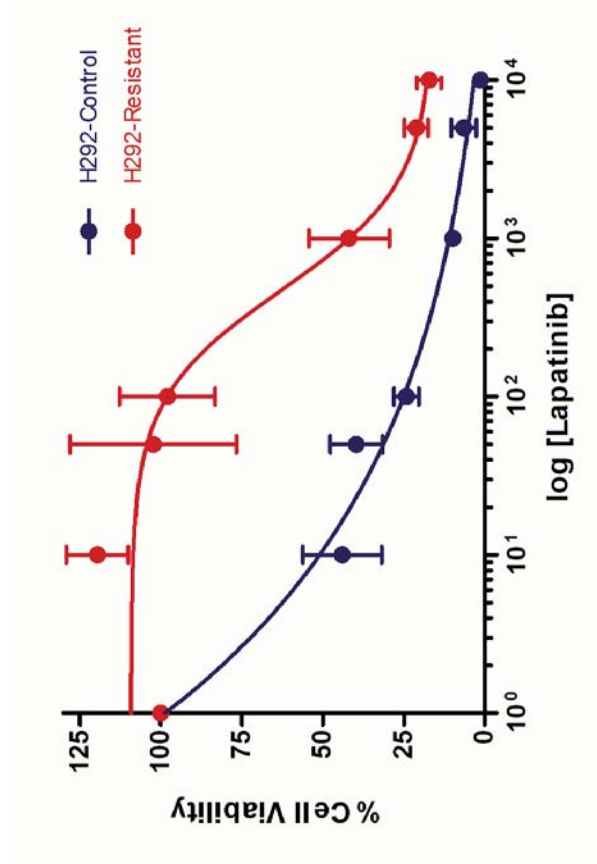
	Replicate 1	Replicate 2	Replicate 3
20 ng	106277100	107386932	
5 ng	108356255	109254315	
1.25 ng	108724000	109124584	
0.31 ng	115500031	121316792	124221951
0.08 ng	125092496	122582478	119270453
0.02 ng	123804788	126355252	123822790

Mean	CV%
116739348	6.58

Western-Blot on Licor Odyssey

Supplementary figure 7: Generation of Lapatinib resistant H292 cells, IC50.

To evoke resistance, H292 cells were cultured in the presence of increasing concentrations of Lapatinib for approximately 7 months. A cell viability assay shows that H292 parental cells are responsive to Lapatinib in the low nanomolar range (IC₅₀ ~ 10nM), whereas resistant cells tolerate 80 fold higher doses (IC₅₀ ~ 800nM).

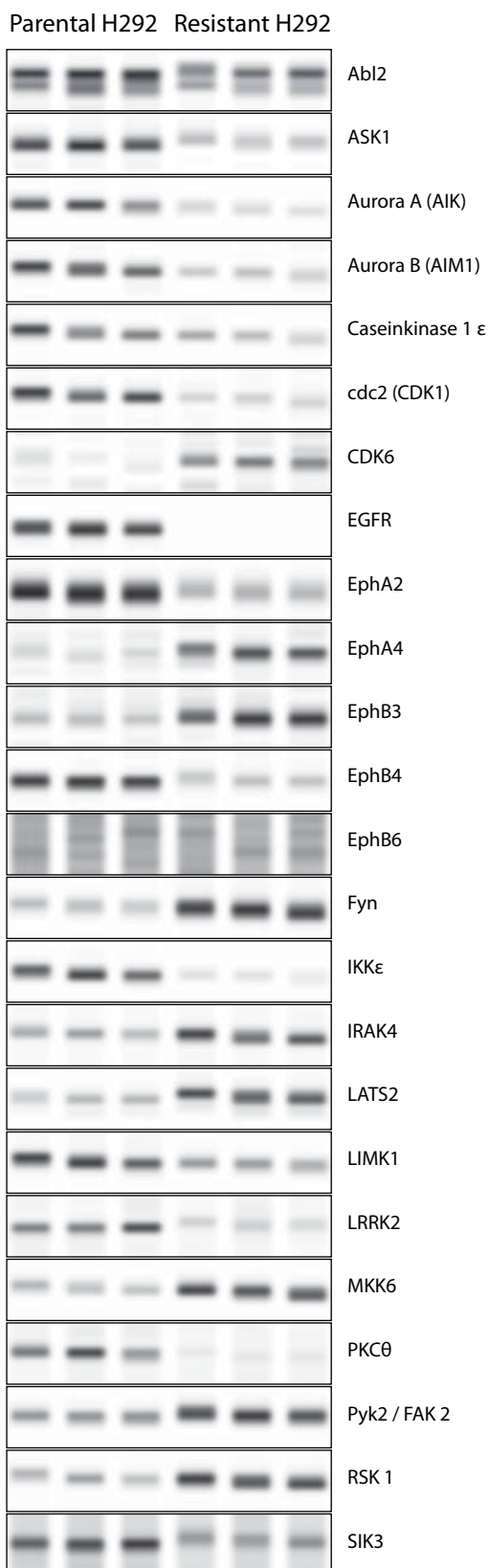


IC₅₀ Control ca. 10nM

IC₅₀ Resistant ca. 800nM

Supplementary figure 8: H292 Lapatinib resistance: Western-Blot mimics of significant kinases.

Western-blot mimics generated from the data obtained on the Kinobead pulldowns from the Lapatinib resistant and the parental H292 cell lysates. Represented are all kinases which are shown in figure 4b and 4c which showed significant changes ($p < 0.01$, $\log_2 > 1$).



Supplementary figure 9: H292 Lapatinib resistance: Canonical pathway and regulator analysis.

Shown are additional details from the Ingenuity pathway analysis for changes in the Lapatinib resistant H292 cell line compared to the parental cell line. Details on the analysis are provided in the methods section. Top canonical pathways associated with the uploaded dataset were extracted. Next, an upstream regulator analysis was performed in order to identify the cascade of upstream transcriptional regulators that are able to explain the observed gene expression changes in our dataset. Given are the top 5 canonical pathways and the top 5 regulators from the analysis.

Regulator Analysis

Top Canonical Pathways		
Name	p-value	Overlap
HER-2 Signaling in Breast Cancer	1.48E-12	10.5 % 8/76
Apoptosis Signaling	4.96E-12	9.1 % 8/88
Molecular Mechanisms of Cancer	4.69E-11	3.1 % 11/359
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	4.49E-10	12.2 % 6/49
Cyclins and Cell Cycle Regulation	7.33E-09	7.8 % 6/77

Top Upstream Regulators	
Upstream Regulator	p-value of overlap
TP53	2.05E-15
FOXM1	6.89E-11
NOTCH1	3.55E-07
BRCA1	1.87E-06
TOP3A	2.99E-06